

RAW SEQUENCE LISTING

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Application Serial Number: 10/564,823
Source: TFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/564,823

TIME: 15:08:36

Input Set : A:\2958-135.txt

Output Set: N:\CRF4\01302006\J564823.raw

3 <110> APPLICANT: Stein, Ulrike
 4 Schwabe, Holger
 5 Walther, Wolfgang
 6 Schlag, Peter Michael
 8 <120> TITLE OF INVENTION: 7a/5 Prognostin and its Use for the Diagnostics and Therapy
 of Tumors
 9
 11 <130> FILE REFERENCE: 2958-135
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/564,823
 C--> 13 <141> CURRENT FILING DATE: 2006-01-18
 13 <150> PRIOR APPLICATION NUMBER: DE 103 32 854.8
 14 <151> PRIOR FILING DATE: 2003-07-18
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP04/008053
 17 <151> PRIOR FILING DATE: 2004-07-19
 19 <160> NUMBER OF SEQ ID NOS: 8
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2559
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 31 gcaaatattga ttgacatgga agctggaaaa ctctcaaaaa gttgcaatat tacagaatgc 120
 33 caggaccag acttgcttca caattggccg gatgctttca cccttcgtgg taataatgct 180
 35 tccaaagtgtg caaatccatt ctggaatcaa ctgtctgctt ctaaccatt tttggatgac 240
 37 ataactcaac taagaaataa caggaagaga aataatat ttccatctaaa ggaagatcct 300
 39 tttcttttct gtagagaaat agaaaatgga aattcttttg attcctccg tgatgaactt 360
 41 gatgtgcatc agttacttag gcagacttcc tcaagaaatt ctggaagatc taaaagtgtt 420
 43 tcagaacttc tggacatttt agacgacaca gcacatgccc atcagagtat acataactct 480
 45 gaccagatcc tactacacga cttagagtgg cttaaaaaatg atcgggaggc ttataaaaatg 540
 47 gcttggttaa gtcaacgcca gctggcccg ccttgccctt atttgaatac aattagtcag 600
 49 agccctggat gggcccagac acaacttgcg gaggtcacca tagcttgcaa agtaaacct 660
 51 caaggagggt cagtacaatt acctgaatca gacatcactg ttcattgtgcc ccaaggatc 720
 53 gtggctgtgg gagaattcca agaggtgtct ctaagggtct tccttgatcc gccacacatg 780
 55 cttaaccatg atctttcgtg cactgtgagc ccgttggtgg aaatcatgtt aggcaacctc 840
 57 aatacaatgg aagccctttt gctggagatg aaaattgggg ctgaagtaag aaagatcct 900
 59 ttcagccaag tcatgacaga aatggtgtgt ttacacagct tgggtaaaaga aggccctttt 960
 61 aaagtittaa gcaactgcta catttataaa gacaccatcc aagtcaagct aatcgacttg 1020
 63 agtcaggtaa tgtatctagt ggttgctgca caagctaaag ctcttccgtc accagctgcc 1080
 65 accatttggg attatatcca caaaaccacc tcaattggaa tttatggacc caaatatctc 1140
 67 catcccagtt ttactgttgt tttaacagtt tgtggacaca attatatgcc aggacagctt 1200
 69 acaatttctg atattaagaa ggggtggaaa aacatatctc cagttgtgtt tcagctctgg 1260
 71 gggaagcagt catttttact tgacaagcca caagatttaa gtatttctat tttttcctgt 1320
 73 gatcctgatt ttgaagtaaa gacagaagga gaaaggaaag aaattaaaca aaagcagttg 1380

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75 gaagcagggtg aagtagttca tcaacaatTT ttatttttctt tagttgagca cagagagatg 1440
77 cacttgtttg atttttgtgt tcaagtggag cctcccaatg gtgaaccagt tgcacagttc 1500
79 tctatcacta ctctgatcc aaccccaaac ctaaaaagac tctcgaatct gccaggctat 1560
81 ttgcagaaga aggaggaaat caagtctgct cctttatcac caaaaattct tgttaaatat 1620
83 cctacatttc aagataaaac attgaacttt agcaactatg gggtaaccct gaaggcagtg 1680
85 ctaagacaaa gcaagattga ttacttcctt gaatatttca aaggggacac aatagctctc 1740
87 ctcggggaag gtaaggtaaa agctattggt cagtccaaag tgaaagaatg gtatgtagga 1800
89 gtcctcagag gtaagattgg acttgtagac tgcaaaaatg tcaaggtgat ttcaaaggag 1860
91 caagtaatgt ttatgtcaga tagtgctttt acaaccagaa atcttcttga acagattgtc 1920
93 ctgcctttta aaaaattgac ttatatctac tcagttgtat taaccttggt gtcagaaaaa 1980
95 gtttatgatt ggaaagtttt agctgatgtc ctgggttact cacatctgtc cctggaagat 2040
97 tttgatcaaa ttcaagcaga caaagaatca gagaaagttt cttatgttat aaagaagtta 2100
99 aaggaagatt gccacacaga gagaaataca aggaagtttc tgtatgaact tattgtggct 2160
101 cttctgaaaa tggattgcca agagttagtc gcacgtctca tccaagaagc tgctgttctg 2220
103 acttcagctg tcaagcttgg aaaaggctgg aggggaactag ctgaaaagtt agtacgactc 2280
105 acaaagcaac aaatggaggc atatgaaatt cctcatcgag gaaacactgg agatgttgct 2340
107 gttgagatga tgtggaaacc tgcctatgat tttctgtata cctggagtgc tcaactatgga 2400
109 aataactaca gagatgtggt acaagacctt cagtcagctt tggacagaat gaaaaaccct 2460
111 gtgactaaac actggagaga attaactgga gttttaatac tagtaaattc tttggaggtt 2520
113 ttgagagtaa ctgcattctc cacttctgag gaagtatag 2559

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116 <210> SEQ ID NO: 2

117 <211> LENGTH: 852

118 <212> TYPE: PRT

119 <213> ORGANISM: Homo sapiens

121 <400> SEQUENCE: 2

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123 Met Leu Ile Thr Glu Arg Lys His Phe Arg Ser Gly Arg Ile Ala Gln
124 1 5 10 15
127 Ser Met Ser Glu Ala Asn Leu Ile Asp Met Glu Ala Gly Lys Leu Ser
128 20 25 30
131 Lys Ser Cys Asn Ile Thr Glu Cys Gln Asp Pro Asp Leu Leu His Asn
132 35 40 45
135 Trp Pro Asp Ala Phe Thr Leu Arg Gly Asn Asn Ala Ser Lys Val Ala
136 50 55 60
139 Asn Pro Phe Trp Asn Gln Leu Ser Ala Ser Asn Pro Phe Leu Asp Asp
140 65 70 75 80
143 Ile Thr Gln Leu Arg Asn Asn Arg Lys Arg Asn Asn Ile Ser Ile Leu
144 85 90 95
147 Lys Glu Asp Pro Phe Leu Phe Cys Arg Glu Ile Glu Asn Gly Asn Ser
148 100 105 110
151 Phe Asp Ser Ser Gly Asp Glu Leu Asp Val His Gln Leu Leu Arg Gln
152 115 120 125
155 Thr Ser Ser Arg Asn Ser Gly Arg Ser Lys Ser Val Ser Glu Leu Leu
156 130 135 140
159 Asp Ile Leu Asp Asp Thr Ala His Ala His Gln Ser Ile His Asn Ser
160 145 150 155 160
163 Asp Gln Ile Leu Leu His Asp Leu Glu Trp Leu Lys Asn Asp Arg Glu
164 165 170 175
167 Ala Tyr Lys Met Ala Trp Leu Ser Gln Arg Gln Leu Ala Arg Ser Cys
168 180 185 190

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171 Leu Asp Leu Asn Thr Ile Ser Gln Ser Pro Gly Trp Ala Gln Thr Gln
172      195      200      205
175 Leu Ala Glu Val Thr Ile Ala Cys Lys Val Asn His Gln Gly Gly Ser
176      210      215      220
179 Val Gln Leu Pro Glu Ser Asp Ile Thr Val His Val Pro Gln Gly His
180 225      230      235      240
183 Val Ala Val Gly Glu Phe Gln Glu Val Ser Leu Arg Ala Phe Leu Asp
184      245      250      255
187 Pro Pro His Met Leu Asn His Asp Leu Ser Cys Thr Val Ser Pro Leu
188      260      265      270
191 Leu Glu Ile Met Leu Gly Asn Leu Asn Thr Met Glu Ala Leu Leu Leu
192      275      280      285
195 Glu Met Lys Ile Gly Ala Glu Val Arg Lys Asp Pro Phe Ser Gln Val
196      290      295      300
199 Met Thr Glu Met Val Cys Leu His Ser Leu Gly Lys Glu Gly Pro Phe
200 305      310      315      320
203 Lys Val Leu Ser Asn Cys Tyr Ile Tyr Lys Asp Thr Ile Gln Val Lys
204      325      330      335
207 Leu Ile Asp Leu Ser Gln Val Met Tyr Leu Val Val Ala Ala Gln Ala
208      340      345      350
211 Lys Ala Leu Pro Ser Pro Ala Ala Thr Ile Trp Asp Tyr Ile His Lys
212      355      360      365
215 Thr Thr Ser Ile Gly Ile Tyr Gly Pro Lys Tyr Ile His Pro Ser Phe
216      370      375      380
219 Thr Val Val Leu Thr Val Cys Gly His Asn Tyr Met Pro Gly Gln Leu
220 385      390      395      400
223 Thr Ile Ser Asp Ile Lys Lys Gly Gly Lys Asn Ile Ser Pro Val Val
224      405      410      415
227 Phe Gln Leu Trp Gly Lys Gln Ser Phe Leu Leu Asp Lys Pro Gln Asp
228      420      425      430
231 Leu Ser Ile Ser Ile Phe Ser Cys Asp Pro Asp Phe Glu Val Lys Thr
232      435      440      445
235 Glu Gly Glu Arg Lys Glu Ile Lys Gln Lys Gln Leu Glu Ala Gly Glu
236      450      455      460
239 Val Val His Gln Gln Phe Leu Phe Ser Leu Val Glu His Arg Glu Met
240 465      470      475      480
243 His Leu Phe Asp Phe Cys Val Gln Val Glu Pro Pro Asn Gly Glu Pro
244      485      490      495
247 Val Ala Gln Phe Ser Ile Thr Thr Pro Asp Pro Thr Pro Asn Leu Lys
248      500      505      510
251 Arg Leu Ser Asn Leu Pro Gly Tyr Leu Gln Lys Lys Glu Glu Ile Lys
252      515      520      525
255 Ser Ala Pro Leu Ser Pro Lys Ile Leu Val Lys Tyr Pro Thr Phe Gln
256      530      535      540
259 Asp Lys Thr Leu Asn Phe Ser Asn Tyr Gly Val Thr Leu Lys Ala Val
260 545      550      555      560
263 Leu Arg Gln Ser Lys Ile Asp Tyr Phe Leu Glu Tyr Phe Lys Gly Asp
264      565      570      575
267 Thr Ile Ala Leu Leu Gly Glu Gly Lys Val Lys Ala Ile Gly Gln Ser

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268          580          585          590
271 Lys Val Lys Glu Trp Tyr Val Gly Val Leu Arg Gly Lys Ile Gly Leu
272          595          600          605
275 Val His Cys Lys Asn Val Lys Val Ile Ser Lys Glu Gln Val Met Phe
276          610          615          620
279 Met Ser Asp Ser Val Phe Thr Thr Arg Asn Leu Leu Glu Gln Ile Val
280 625          630          635          640
283 Leu Pro Leu Lys Lys Leu Thr Tyr Ile Tyr Ser Val Val Leu Thr Leu
284          645          650          655
287 Val Ser Glu Lys Val Tyr Asp Trp Lys Val Leu Ala Asp Val Leu Gly
288          660          665          670
291 Tyr Ser His Leu Ser Leu Glu Asp Phe Asp Gln Ile Gln Ala Asp Lys
292          675          680          685
295 Glu Ser Glu Lys Val Ser Tyr Val Ile Lys Lys Leu Lys Glu Asp Cys
296          690          695          700
299 His Thr Glu Arg Asn Thr Arg Lys Phe Leu Tyr Glu Leu Ile Val Ala
300 705          710          715          720
303 Leu Leu Lys Met Asp Cys Gln Glu Leu Val Ala Arg Leu Ile Gln Glu
304          725          730          735
307 Ala Ala Val Leu Thr Ser Ala Val Lys Leu Gly Lys Gly Trp Arg Glu
308          740          745          750
311 Leu Ala Glu Lys Leu Val Arg Leu Thr Lys Gln Gln Met Glu Ala Tyr
312          755          760          765
315 Glu Ile Pro His Arg Gly Asn Thr Gly Asp Val Ala Val Glu Met Met
316          770          775          780
319 Trp Lys Pro Ala Tyr Asp Phe Leu Tyr Thr Trp Ser Ala His Tyr Gly
320 785          790          795          800
323 Asn Asn Tyr Arg Asp Val Leu Gln Asp Leu Gln Ser Ala Leu Asp Arg
324          805          810          815
327 Met Lys Asn Pro Val Thr Lys His Trp Arg Glu Leu Thr Gly Val Leu
328          820          825          830
331 Ile Leu Val Asn Ser Leu Glu Val Leu Arg Val Thr Ala Phe Ser Thr
332          835          840          845
335 Ser Glu Glu Val
336          850

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339 <210> SEQ ID NO: 3

340 <211> LENGTH: 21

341 <212> TYPE: DNA

342 <213> ORGANISM: Homo sapiens

344 <400> SEQUENCE: 3

345 ttcttttgat tctccggtg a

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348 <210> SEQ ID NO: 4

349 <211> LENGTH: 20

350 <212> TYPE: DNA

351 <213> ORGANISM: Homo sapiens

353 <400> SEQUENCE: 4

354 actctgatgg gcatgtgctg

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357 <210> SEQ ID NO: 5

358 <211> LENGTH: 32

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359 <212> TYPE: DNA
360 <213> ORGANISM: Homo sapiens
362 <400> SEQUENCE: 5
363 gcagacttcc tcaagaaatt ctggaagatc ta 32
366 <210> SEQ ID NO: 6
367 <211> LENGTH: 32
368 <212> TYPE: DNA
369 <213> ORGANISM: Homo sapiens
371 <400> SEQUENCE: 6
372 agtgtttcag aacttctgga catttttagac ga 32
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
378 <213> ORGANISM: Homo sapiens
380 <400> SEQUENCE: 7
381 aagcttggaa aaggctggag g 21
384 <210> SEQ ID NO: 8
385 <211> LENGTH: 18
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens
389 <400> SEQUENCE: 8
391 Lys Leu His Ser Ala Leu Asp Arg Met Lys Asn Pro Val Thr Lys His
392 1 5 10 15
395 Trp Arg

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/564,823

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Input Set : A:\2958-135.txt

Output Set: N:\CRF4\01302006\J564823.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date